

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: July 18, 2001, 15:58:17 ; Search time 12.89 Seconds
(without alignments)
2030.348 Million cell updates/sec

Title: US-09-587-111-5

Perfect score: 4004
1 MTPSSSPVRLFTLDGGQE.....EDEDGASEENVYPVLLQSN 764

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|--------------|---------------------|
| 1 | 215 | 5.4 | 973 | 1 TRP5_HUMAN | Q9UL62 homo sapien |
| 2 | 198.5 | 5.0 | 1275 | 1 TRP_DROME | P19334 drosophila |
| 3 | 197.5 | 4.9 | 1124 | 1 TRPL_DROME | P48994 drosophila |
| 4 | 159 | 4.0 | 809 | 1 TRP1_MOUSE | O61056 mus musculus |
| 5 | 151 | 3.8 | 3924 | 1 ANK2_HUMAN | O01484 homo sapien |
| 6 | 150.5 | 3.8 | 793 | 1 TRP1_HUMAN | P48995 homo sapien |
| 7 | 140 | 3.5 | 1862 | 1 ANK1_MOUSE | O02357 mus musculus |
| 8 | 139 | 3.5 | 848 | 1 TRP3_HUMAN | Q13507 homo sapien |
| 9 | 138 | 3.4 | 1880 | 1 ANK1_HUMAN | P16157 homo sapien |
| 10 | 134.5 | 3.4 | 1401 | 1 LATA_LATMA | P23631 latrodectus |
| 11 | 133.5 | 3.3 | 642 | 1 YAZA_SCHPO | O09701 schizosacch |
| 12 | 130 | 3.2 | 930 | 1 TRP6_MOUSE | O61143 mus musculus |
| 13 | 129 | 3.2 | 1964 | 1 NTC4_MOUSE | P31695 mus musculus |
| 14 | 128.5 | 3.2 | 1093 | 1 SWI4_YEAST | P25302 saccharomyc |
| 15 | 124.5 | 3.1 | 2703 | 1 NOTC_DROME | P07207 drosophila |
| 16 | 123.5 | 3.1 | 832 | 1 ANR3_HUMAN | O03017 drosophila |
| 17 | 123 | 3.1 | 500 | 1 CACT_DROME | O94759 homo sapien |
| 18 | 121.5 | 3.0 | 1503 | 1 TRP7_HUMAN | O9Y210 homo sapien |
| 19 | 121 | 3.0 | 931 | 1 TRP6_HUMAN | Q05823 homo sapien |
| 20 | 120.5 | 3.0 | 741 | 1 RN5A_HUMAN | P24586 caenorhabdi |
| 21 | 120.5 | 3.0 | 823 | 1 RN52_CAEEL | P35364 rattus norv |
| 22 | 119.5 | 3.0 | 357 | 1 SH5A_RAT | P41412 schizosacch |
| 23 | 119 | 3.0 | 657 | 1 RES2_SCHPO | O9ZCZ1 mus musculus |
| 24 | 119 | 3.0 | 836 | 1 TRP3_MOUSE | Q22566 caenorhabdi |
| 25 | 117.5 | 2.9 | 613 | 1 XSV1_CAEEL | P30966 mus musculus |
| 26 | 116 | 2.9 | 357 | 1 SH5A_MOUSE | P14585 caenorhabdi |
| 27 | 115 | 2.9 | 1429 | 1 L112_CAEEL | P25799 mus musculus |
| 28 | 113 | 2.8 | 971 | 1 KBF1_MOUSE | O60733 homo sapien |
| 29 | 112.5 | 2.8 | 806 | 1 PA26_HUMAN | O00748 drosophila |
| 30 | 112 | 2.8 | 1302 | 1 MDR5_DROME | O61982 mus musculus |
| 31 | 112 | 2.8 | 2318 | 1 NTC3_MOUSE | P39010 saccharomyc |
| 32 | 111.5 | 2.8 | 764 | 1 AKR1_YEAST | P40480 saccharomyc |
| 33 | 111.5 | 2.8 | 1083 | 1 YIL2_YEAST | |

| | | | | | |
|----|-------|-----|------|--------------|---------------------|
| 34 | 111.5 | 2.8 | 2444 | 1 NTC1_HUMAN | P46531 homo sapien |
| 35 | 111 | 2.8 | 637 | 1 RES1_SCHPO | P33520 schizosacch |
| 36 | 110.5 | 2.8 | 538 | 1 THIP_HAEN | P44985 haemophilus |
| 37 | 110.5 | 2.8 | 1431 | 1 DAPK_HUMAN | P53355 homo sapien |
| 38 | 109.5 | 2.7 | 906 | 1 KBF2_CHICK | P68150 gallus gall |
| 39 | 109.5 | 2.7 | 2353 | 1 CCAH_HUMAN | O05180 homo sapien |
| 40 | 109.5 | 2.7 | 2531 | 1 NTC1_RAT | O07008 rattus norv |
| 41 | 109 | 2.7 | 1873 | 1 CCAS_RABIT | P07293 oryctolagus |
| 42 | 108.5 | 2.7 | 448 | 1 NU4M_ANOU | P33511 anopheles g |
| 43 | 108.5 | 2.7 | 2437 | 1 NOTC_BRARE | P46530 brachydanio |
| 44 | 107.5 | 2.7 | 614 | 1 GAAL_YEAST | P39012 saccharomyc |
| 45 | 107.5 | 2.7 | 679 | 1 RN5A_MOUSE | Q05921 mus musculus |

ALIGNMENTS

| RESULT | 1 | TRP5_HUMAN | STANDARD | PRT | 973 AA |
|--------|--|------------|----------|-----|-----------------------------------|
| ID | TRP5_HUMAN | | | | |
| AC | Q9UL62; | | | | |
| DT | 01-OCT-2000 (Rel. 40, Created) | | | | |
| DT | 01-OCT-2000 (Rel. 40, Last sequence update) | | | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | | | |
| DE | TRANSIENT RECEPTOR POTENTIAL CHANNEL 5 (HTRP-5). | | | | |
| GN | TRPC5 OR TRP5. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RN | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Brain; | | | | |
| RX | MEDLINE=99425273; PubMed=10493832; | | | | |
| RA | Sossey-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J., | | | | |
| RA | Hane B., Schwartz C.E., Stevenson R.E., Srivastava A.K.; | | | | |
| RT | "Molecular cloning and characterization of TRPC5 (HTRP5), the human | | | | |
| RT | homologue of a mouse brain receptor-activated capacitative Ca(2+) | | | | |
| RT | entry channel."; | | | | |
| RL | Genomics 60:330-340(1999). | | | | |
| CC | -!- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE). | | | | |
| CC | -!- SEEMS TO FORM A CALCIUM PERMEANT CHANNEL. | | | | |
| CC | -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL). | | | | |
| CC | -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. | | | | |
| CC | -!- SIMILARITY: CONTAINS 2 ANK REPEATS. | | | | |
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| CC | or send an email to license@isb-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL; AF054568; AF00002.1; - | | | | |
| DR | InterPro: IPR002110; - | | | | |
| DR | InterPro: IPR002111; - | | | | |
| DR | InterPro: IPR002153; - | | | | |
| DR | Pfam: PF00023; ank. 2. | | | | |
| DR | PRINTS; PRO1097; TRANSMEMBRANE; Ion transport; Calcium channel; | | | | |
| DR | IONIC channel; Transmembrane; Ion transport; Calcium channel; | | | | |
| KW | ANK repeat; Repeat; Glycoprotein. | | | | |
| FT | TRANSMEM 331 351 | | | | POTENTIAL. |
| FT | TRANSMEM 364 384 | | | | POTENTIAL. |
| FT | TRANSMEM 399 419 | | | | POTENTIAL. |
| FT | TRANSMEM 438 458 | | | | POTENTIAL. |
| FT | TRANSMEM 471 491 | | | | POTENTIAL. |
| FT | TRANSMEM 513 533 | | | | POTENTIAL. |
| FT | TRANSMEM 568 588 | | | | POTENTIAL. |
| FT | TRANSMEM 604 624 | | | | POTENTIAL. |
| FT | REPEAT 69 98 | | | | ANK 1. |
| FT | REPEAT 141 170 | | | | ANK 2. |
| FT | REPEAT 91 91 | | | | N-LINKED (GLCNAC. .) (POTENTIAL). |
| FT | CARBOHYD 91 91 | | | | |

FT CARBOHYD 461 461 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 678 678 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 900 900 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 973 AA; 111411 MW; FBC8CBF17BE42166 CRC64;

Query Match 5.4%; Score 215; DB 1; Length 973;
 Best local similarity 20.5%; Pred. No. 1e-07;
 Matches 162; Conservative 115; Mismatches 278; Indels 234; Gaps 36;

QY 122 KAVLN-LKDGVAACILPLAIDIDSGNPPVNAOCTDYRHSALHIAIEKRSIQCVK 180
 DB 34 KALINVEKGDYATVQAQAEIYYN---VINCMDDP--GRSALLIAIEMENLEIME 87
 QY 181 LTVENGANV-----HARACGRFGKGGTGC---YFGEL-----211
 DB 88 LLINHSYVGDALLYAIRKVVAGAVELLISYRPSG---EKQVPTLMMDTQSEFPDIT 144
 QY 212 PLSLAACKOMDVSVYLE-----NPHOPASLOATDSQGNVLAHALVMSIDSAENIAL 265
 DB 145 PIMLAHTNNEYELIKLVQKRVITPRHQ-----IRCNCECVS- 183
 QY 266 VTSMTGOLLAQARLCPTVOLIEDIRNLODTPKLAKKEGKIEIFRIILORESGISHLS 325
 DB 184 -SSEVDSLRSR-----LNTYKALASPSLALSEDEPILTAFR--LGMELKELSKVE 234
 QY 326 RKF-TEWCYGPVAVSLYDLASVDSCEENSVLEIIFH-----CK 363
 DB 235 NEKAEYEELSOQCKLFKAKLLOQARSRELEIILNRDHSLEDPQKHDIAKLKVAL 294
 QY 364 SPHRHRVYLEPIKLLQAKN-----384
 DB 295 KYHQKEVQAPNCOQLATLWYDGPQRRKHWVLLTCTIGLEFPLMSTAVLISPRS 354
 QY 385 -DLIPKPIANLCN---LIYFIFTAVAH--OPTLKKQAAPHKAEGVSMILTG 436
 DB 355 NLGLFKPKPIKICHTASYLTFLFLLASOHIVRTDLHVGPPPTVVE--WMLLPW- 410
 QY 437 ILILGIVLYVGLW-YFRRHVFIVISFIDSYFELLFQALLTVVSGVLCFLAIE-- 493
 DB 411 -VLGPIWKEIKEMDGTETIHDMMNLMDFAMNSLY---LATISLKIYAVKYNCS 463
 QY 494 -----WTLPLVLSAL-----VLGMLNLVYTRGFOHTGIYSVMIOKYLRLLELL 540
 DB 464 RPREMEMHPTLIAELFAISNLSLRISLFTANSHLQDISGRMLL-DILKFLF 522
 QY 541 IYVFLFGFVALVLSQEAHREAPRGPAATESVOPMEQDEBGNCAQYRGILLEASLEL 600
 DB 523 IYCLVLIAFANGLNOL-YFYETRAIDEPNNCKGIR---CEKQNNNA--FSTLEFLOSL 575
 QY 601 FKFTIGMGL-----AFQOLHFRGVLLLLLAAYVLLTLLNMLIALMSETVSVAT 654
 DB 576 FMSVFGILNLYVNVKARHETFEVGAT--MFGTYNVISLVLLNMLIAMMNSYQILAD 633
 QY 655 DSKSINKLQKA---ISVLE-----MENGVY---WCKRKORAGVMT 669
 DB 634 HADIEKFKATKLMASYDEGTLPPFPNIIPSPKSFLYLGNMFMNFTCPKRD----- 686
 QY 690 VGRKPGSGPDERKCFRVEEVNNAW--EQTLPTICEBPSGAGVPTLENPLASPKDE- 747
 DB 687 ----PGRRRRR-----NLSRFTERNADSLIONOHVOEIVRLNKRYVAAMIRSKT 734
 QY 748 -DGASEENY 755
 DB 735 HEGLTENN 743

DT 01-NOV-1995 (rel. 32, last sequence update)
 DT 01-OCT-2000 (rel. 40, last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL PROTEIN.
 GN TRP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OREGON-R;
 RX MEDLINE=90180449; PubMed=2516726;
 RA Montell C., Rubin G.M.;
 RT Molecular characterization of the Drosophila trp locus: a putative
 RT integral membrane protein required for phototransduction.;
 RL Neuron 2:1313-1323(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148782; PubMed=2482778;
 RA Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,
 RA Shao D.;
 RT *Proper function of the Drosophila trp gene product during pupal
 RT development is important for normal visual transduction in the
 RL adult.*;
 RN Neuron 3:81-94(1989).
 RN [3]
 RP SEQUENCE OF 1126-1275 FROM N.A.
 RX MEDLINE=88042982; PubMed=3118483;
 RA Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
 RT Overlapping transcription units in the transient receptor potential
 RT locus of Drosophila melanogaster.;
 RL Somat. Cell Mol. Genet. 13:661-669(1987).
 CC - FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
 CC CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
 CC CHANNEL.
 CC - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC - TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
 CC - SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC - SIMILARITY: CONTAINS 2 ANK REPEATS.
 CC -----
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 CC EMBL: M34394; AAA28976.1; -
 CC EMBL: M21306; AAA56928.1; -
 CC EMBL: M18634; AAA28977.1; -
 CC PIR: J00092; J00092.
 CC PIR: J00015; J00015.
 CC Flybase: FBgn0003861; trp.
 CC InterPro: IPR002110; -
 CC InterPro: IPR002153; -
 CC Pfam: PF00023; ank. 1.
 CC PRINTS: PR01097; TRNSRECEPTR.
 CC PROSITE: PS50088; ANK_REPEAT. 1.
 CC PROSITE: PS50297; ANK_REPEAT_REGION. 1.
 CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW Vision; ANK repeat; Repeat.
 FT TRANSMEM 334 354
 FT TRANSMEM 378 401
 FT TRANSMEM 419 436
 FT TRANSMEM 457 471
 FT TRANSMEM 504 527
 FT TRANSMEM 612 630
 FT TRANSMEM 636 661
 FT TRANSMEM 69 98
 FT REPEAT 143 172
 FT ANK 1.
 FT ANK 2.

QY 384 MDLIPKFLNLCN-----LIYMFITFAVA-----YHOPFLKQQAAPHLKAEVGN 429
 DB 366 TQGLMKRPKPKFLHASSYFLFLILVYSQADDDFVRIFGTTRMKKELAEQELRQCG 425
 QY 430 SMLTGHILLIGITLVAGQWYFMRHAFIMISFIDSFELLFLFOALL--TVYSQVL 487
 DB 426 ----TFSKLELIYMYV---IGFWEEVOELFVAGKSKYLRRNMNMTDLRNSLYSVM 477
 QY 488 CFLAIEW-----YLP-----LLVASLVGWLNLVYTRGFQ 518
 DB 478 CLAFAYIQGATEIARDPOKAYIPREKMHDFDQLAEGFLAANAYFSALKLVHLSINP 537
 QY 519 HTGITYSMIOKVLRLDLRLLLVYFLFGFANALVLSQEA-----RPEAPGPNAT 572
 DB 538 HLPGLIISLRMYI-DIVKFFFLYTLVLFIFA---CGLNOLWYFALERSKCYVLPFG-- 591
 QY 573 ESYQPMGDEBNGA-----QYRGILEASLELFFFTIGMGL-----ARQEOQLHFR 619
 DB 592 -----GEADKSHGSDCKMRFRGNLFESSOSLTFWASGAMGLDFELSGIKSTTRFW 644
 QY 620 GAVLLLLLAVLLTYLLMLTALMSEVNSVATDSWISWIKLQKAISVLEMENGYWCR 679
 DB 645 G-LMEGYSVINVITVLLMLTAMMSNSYAMIDEHSDETKFAR-----TKLMSY 694
 QY 680 KKRAGVMLTVGKPDGSPDERMCFV-----EEYNWASWQTLPTLC 722
 DB 695 FEDSA---TLPPFVNLPSVKWVIRIFRKSXTIDRQSKRKEQEFQSEYDINIKSLV 750
 QY 723 EDPSGAVPRTLENPVLASPKDE--DGASENVYVYOLLO 762
 DB 751 W-RYVAAMHKKFEN---NVSSEDINEVSEINTMYEMLE 787

RESULT 4
 TRPL_MOUSE STANDARD: PRT: 809 AA.
 AC 061056; 035722; 40, Created)
 DT 01-OCT-2000 (Rel. 40, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE TRANSLATION RECEPTOR POTENTIAL CHANNEL 1 (TRANSLATION RECEPTOR PROTEIN 1)
 GN (MTRP1) (TRP-RELATED PROTEIN 1).
 OS TRP1 OR TRP1 OR TRP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Insulinoma;
 RC MEDLINE=97307994; PubMed=9165220;
 RA Sakura H., Ashcroft F.M.;
 RT Identification of four trp1 gene variants murine pancreatic beta-
 RT cells".
 RL Diabetologia 40:528-532(1997).
 RN [2]
 RP SEQUENCE FROM N.A. (BETA ISOFORM).
 RC TISSUE=Lens epithelium;
 RA Rae J.L.;
 RT "Ion channels in lens epithelia".
 RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 551-615 FROM N.A.
 RA MEDLINE=96234226; PubMed=8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT "A novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RL Cell 85:661-671(1996).
 CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA; ARE

PRODUCED BY ALTERNATIVE SPLICING.
 -1- SIMILARITY: BELONGS TO THE TRANSLATION RECEPTOR FAMILY.
 -1- SIMILARITY: CONTAINS 3 ANK REPEATS.
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DR EMBL: U73625; AAB50622.1; -
 DR EMBL: U95167; AAC53162.1; -
 DR EMBL: AF191551; AAF05725.1; -
 DR EMBL: U40980; AAC52699.1; -
 DR MGD: MG1:109528; Trp1.
 DR InterPro: IPR002113; -
 DR InterPro: IPR002153; -
 DR PRINTS: PRO1097; TRANSMEMBRP.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KW ANK repeat; Repeat; Alternative splicing.
 FT TRANSMEM 367 423 POTENTIAL.
 FT TRANSMEM 403 423 POTENTIAL.
 FT TRANSMEM 432 452 POTENTIAL.
 FT TRANSMEM 512 532 POTENTIAL.
 FT TRANSMEM 556 576 POTENTIAL.
 FT TRANSMEM 603 623 POTENTIAL.
 FT TRANSMEM 633 653 POTENTIAL.
 FT REPEAT 62 91 ANK 1.
 FT REPEAT 99 128 ANK 2.
 FT REPEAT 174 203 ANK 3.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 597 597 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 126 159 MISSING (IN ISOFORM BETA).
 SQ SEQUENCE 809 AA; 92727 MW; DFD8377D5C538CDD CRC64;

Query Match 4.0%; Score 159; DB 1; Length 809;
 Best local Similarity 18.8%; Pred. No. 0.00083;
 Matches 142; Conservative 115; Mismatches 249; Indels 248; Gaps 34;

QY 86 GVEDIAGLPEY-----LSKTSKYLTDESEYEGSGTKCLMKAV----- 124
 DB 2 GAPPSPGLPPSNAMMALYPSTDLGVSSSSPSSSPSSSPNEVMALKDVEVKEENT 61
 QY 125 LNKDGVNAC-----ILPLQIDRDGSGNPPVNAOCTDYYRGHSALHAIERRSIQ 177
 DB 62 LNEKFLFLACDKGDYVWKKILE-ENSSGD---LNIQVND-VLGRNAVITITENESID 114
 QY 178 CAVLVENAGN-----VHARAGC-----RFGQGGCGCFRFG----- 210
 DB 115 ILQLLDYCGQSADALLVAIDSEVGAVDILNHRKRSRPTIVKMERIONPEYSTM 174
 QY 211 --LPLSLACTKQMDVSVYLE--NPH----- 233
 DB 175 DVAPVILAAHRNNYEITLMLLKQDVSLEPRHANGCCTCSAKNKKDSLHRSFRDIYR 234
 QY 234 ---QPASIQATDSQNTVLAHVMISD-----NSAENIALVTSMYDGLLQQA 278
 DB 235 CLASPALIMTEE--DPIILAFELADKELSLVEFEFRNDYEELARQCKMFKADLLQA 292
 QY 279 RLCPTVQLEDIRN-----LQDITPLKLAKEKIEIFRHHIIORESGSL 322
 DB 293 R--NSRELEVILNHTSSDEPLDKGLLEBRMNLRLKLAIKTN-----QKE- 337
 QY 323 HLSRKTEMCYGVAVSLVDIASVDSCEENSVLEIAPFCKSPHRH-----MVLE-- 374
 DB 338 -----VSQSNCOQ--PLNTYWFQMSGYSRRKPKCKIMYLVTVG 374

QY 375 ---PUNKIL-----QAKWDLIPKFEFLNCLNIYMEFT-----AVAYHQPPLKKQAA 420
DQ 375 IFMVLSTCYLIAPKSOFGRIHPTPEMFIHGASYSFELLNLYSLVNEDEK----- 428
QY 421 PHLAEVNSNLLGHILLGLGTYLVGLMVFMRHVFMTWISIDSYFE-----ILFL 475
DQ 429 ---NFMKPALERIDYLLIL-----WIIGMTWSDIKR---LMYEGLEDPEESRNQSLSFV 477
QY 476 FQA---LLTVVSOVLCEFLAI-----EW---YLPLLSALVGLMNLLYTGTGFGHTGIS 524
DQ 478 MNSLYLAFALKVVAHNKHFADRKMDAPHPLVAGLEAFANVLSYLLFMYTTSS 537
QY 525 VM-----IQKYLRLDLLELLIYVLEFGAVALVSLSQEAMRPAPTGPMTATESVDME 579
DQ 538 ILGLPLQISMGMQLADFGKFLMFLVLEFSLFTIGLTQDKGY-----TSKQKDCVGFIC 592
QY 580 GQDEGNGAQYRGILSELSLEKFTIGMGLAF-----QEQULHFGWMLLLLAIVL 631
DQ 593 EQQSNDR---FHSFTGTCFALEWYFSLAHVAIVTRPSYGELOSFGAV--IVGTYNV 647
QY 632 LTYILLNMLIALMSEYVNSVATDSWSIMKLOKA 665
DQ 648 VVIVLTVFKLVAMLMKRSQOLLANHDEKMKRARA 681
RESULT 5
ANK2_HUMAN ID ANK2_HUMAN STANDARD; PRT: 3924 AA.
AC 001484: 001485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
GN ANK2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE-Brain stem;
RA MEDLINE=94075409; PubMed=8253844;
RT Chan W., Kordell E., Bennett V.,
RT "440-kD ankyrin: structure of the major developmentally regulated
RT domain and selective localization in unmyelinated axons.";
RT J. Cell Biol. 123:1463-1473(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE-Brain stem;
RA MEDLINE=91302466; PubMed=1830053;
RT Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
RT ankyrins reveal a family of alternatively spliced genes.";
RT J. Cell Biol. 114:241-253(1991).
RN [3]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RA MEDLINE=92009921; PubMed=1833308;
RT Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
RA Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel noneythrind
RT ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
CC SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
CC BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
CC AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
CC DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
CC THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.

CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CC CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
CC AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
CC AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
DR EMBL; Z26634; CAB42644.1; -
DR EMBL; X56957; CAA40278.1; -
DR EMBL; X56958; CAA40279.2; -
DR EMBL; M37123; AAA62828.1; -
DR PIR; S14533; S14533.
DR PIR; A39643; A39643.
DR PIR; B39643; B39643.
DR PIR; S14569; S14569.
DR HSP; 000420; IABC.
DR MIM; 106410; -
DR InterPro; IPR000488; -
DR InterPro; IPR000906; -
DR InterPro; IPR002110; -
DR Pfam; PF00791; Z05; 1.
DR Pfam; PF00023; ank; 22.
DR Pfam; PF00531; death; 1.
DR PROSITE; PSS0088; ANK_REPEAT; 20.
DR PROSITE; PSS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PSS0017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation; Multigene family.
FT REPEAT 63 92 ANK 1.
FT REPEAT 96 125 ANK 2.
FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
FT REPEAT 331 360 ANK 9.
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| FT | REPEAT | 1892 | 1902 | REPEAT A (APPROXIMATE). |
| FT | REPEAT | 1903 | 1914 | REPEAT A. |
| FT | REPEAT | 1915 | 1926 | REPEAT A. |
| FT | REPEAT | 1927 | 1938 | REPEAT A. |
| FT | REPEAT | 1939 | 1950 | REPEAT A. |
| FT | DOMAIN | 3536 | 3620 | DEATH DOMAIN. |
| FT | VARSPLIC | 1039 | 1039 | O -> QPGLKHLPTAPPLNIGESLVSRIILQGPPTK (IN ISOFORM 2). |
| FT | VARSPLIC | 1444 | 3528 | MISSING (IN ISOFORM 2 AND ISOFORM 3). |
| FT | CONFLICT | 475 | 476 | GO -> PE (IN REF. 4). |
| FT | CONFLICT | 971 | 971 | I -> S (IN REF. 2). |
| FT | CONFLICT | 3581 | 3582 | OY -> HA (IN REF. 2). |
| FT | CONFLICT | 3586 | 3586 | I -> Y (IN REF. 2). |
| SO | SEQUENCE | 3924 AA; | 430337 | MM; 52AC496C428E9D2 CXC64; |

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| Query Match | 3.88; | Score 151; | DB 1; | Length 3924; |
| Best Local Similarity | 27.38; | Pred. No. 0.024; | | |
| Matches 88; | Conservative 46; | Mismatches 96; | Indels 92; | Gaps 19 |

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| QY | 139 | LOIDRSDSNPPIVNAOCTDDYUHGSHLHAIKRSIOCKLILVENGAVNHAACRFE | 198 |
| QY | 139 | LOIDRSDSNPPIVNAOCTDDYUHGSHLHAIKRSIOCKLILVENGAVNHAACRFE | 198 |
| Db | 383 | LLDOK-RANP---NARALN---GPRPLHACKKNRIKVELLVKXGASIOA----- | 426 |
| QY | 199 | OKGOSTCYBEELPLSLAACKTHQDVSYLEENHOPASLOATDSCGNTYUHALVMSDN | 258 |
| Db | 427 | -----ITESLITPRHVAAMFGHINIVILLON---GASPDVTNIRIBETALHMA----- | 472 |
| QY | 259 | SAENIALVTSMYDGLGAGARICPTVOLEDIRNODLTPLEKLAKEGKIEIFRIHLOEF | 318 |
| Db | 473 | RAGQEVVRC-----LLRNGA-----LVDAAREBQTPPHIARSLRKLTEIYQLOLGH-- | 519 |
| QY | 319 | SGLSLSLKRFTKEMCYGPRVSL-----YDLASVDSCEENSYLEIIAIFCKSCHHRRMYLE | 374 |
| Db | 520 | --MAIPDAATNG--YTPPHISAREQYDVASV-----LLEAGAAHSLATKKG---FT | 565 |
| QY | 375 | PLNKLLOAKMDL-IPKFEFL-----NPLCNLIYMFIEFAVAVYHOPT-----L | 415 |
| Db | 566 | PLH--VAAKYGSLOVAKLLDGRRAADSAGKNGLTPL-----HYAAHNDQNCVALLL | 616 |
| QY | 416 | KKOAPPHLKAIEVNSMLLTGHI | 437 |
| Db | 617 | EKGASPHATAKNGYTPL---HI | 635 |

| | RESULT | 6 |
|------------|--|------------------------|
| TRP1_HUMAN | | |
| ID | TRP1_HUMAN | STANDARD; PRT; 793 AA. |
| AC | PA8995; | |
| DT | 01-FEB-1996 (Rel. 33, Created) | |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update) | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | |
| DE | TRANSPORT RECEPTOR POTENTIAL CHANNEL 1 (TRP-1 PROTEIN) (TRPCL | |
| DE | PROTEIN). | |
| GN | TRPCL OR TRP1. | |
| OS | Homo sapiens (Human). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | |
| OX | NCBI_TaxId=9606; | |
| RN | [1] | |
| RP | SEQUENCE FROM N.A. | |
| RX | MEDLINE=96033971; PubMed=7589464; | |
| RA | Zhu X., Chu P.B., Peyton M., Birnbaumer L.; | |
| RT | "Molecular cloning of a widely expressed human homologue for the | |
| RL | Drosophila tip gene."; | |
| | FEBS Lett. 373:193-198(1995). | |

RN 121
 RP SEQUENCE FROM N.A. (SHORT FORM).
 RC TISSUE=Brain;
 RX MEDLINE=96003837; PubMed=7568191;
 RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,
 RT Montell C.;
 "TRPC1, a human homolog of a Drosophila store-operated channel."

```

RL Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).
RN [3]
RP SEQUENCE FROM N.A. (SHORT FORM).
RC TISSUE=Brain;
RX MEDLINE=96258271; Pubmed=8663995;
RA Zitt C., Zobel A., Obukhov A.G., Harteneck C., Kalkbrenner F.,
RA Lueckhoff A., Schultz G.;
RT "Cloning and functional expression of a human Ca2+-permeable cation
RT channel activated by calcium store depletion.";
RL Neuron 16:1189-1196(1996).
CC
CC -I- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
CC
CC SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.
CC
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC
CC -I- TISSUE SPECIFICITY: SEEMS TO BE UBICUITOUS.
CC
CC -I- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
CC
CC -I- SIMILARITY: CONTAINS 3 ANK REPEATS.
CC
CC -----
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| | | | | |
|----|---|------------|---------------|-------------------------------------|
| DR | EMBL: | U31110; | AAA93251.1; | - |
| DR | EMBL: | U31101; | AAA93252.1; | - |
| DR | EMBL: | X89066; | CAA61447.1; | - |
| DR | EMBL: | Z73903; | CAA98108.1; | - |
| DR | MIM: | 602343; | - | - |
| DR | InterPro: | IPRO02153; | - | - |
| DR | PRINTS: | PRT01097; | TRANSRECEPTR. | |
| KW | Ionic channel; Transmembrane; Ion transport; Calcium channel; | | | |
| KW | ANK repeat; Repeat; Alternative splicing. | | | |
| FT | TRANSMEM | 351 | 371 | POTENTIAL. |
| FT | TRANSMEM | 387 | 407 | POTENTIAL. |
| FT | TRANSMEM | 416 | 436 | POTENTIAL. |
| FT | TRANSMEM | 458 | 475 | POTENTIAL. |
| FT | TRANSMEM | 540 | 560 | POTENTIAL. |
| FT | TRANSMEM | 587 | 607 | POTENTIAL. |
| FT | TRANSMEM | 617 | 637 | POTENTIAL. |
| FT | REPEAT | 46 | 75 | ANK 1. |
| FT | REPEAT | 83 | 112 | ANK 2. |
| FT | REPEAT | 158 | 187 | ANK 3. |
| FT | CARBOHYD | 70 | 70 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 287 | 287 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 306 | 306 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD | 581 | 581 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC | 110 | 143 | MISSING (IN SHORT ISOFORM). |
| SQ | SEQUENCE | 793 AA; | 91211 MW; | FACC7GADDFFA320AE CRC64; |

| | | | | |
|-----------------------|------------------|------------------|------------|------------|
| Query Match | 3.8% | Score 150.5 | DB 1 | Length 793 |
| Best Local Similarity | 18.7% | Pred. No. 0.0033 | | |
| Matches 136 | Conservative 116 | Mismatches 242 | Indels 235 | Gaps 33 |

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QY 98 LSTKSKYLLDSEYEGSTGKTCLMKAV-----LMLKQVNAAC-----ILPLQID 142
Db 11 LSGASSSLSPSPSSSPSPNEVMALKDVBREKREENTLLEKLELLACDKGDYVWKLE-E 69
QY 143 RDSGNPOLVNAOCTDDYVNGSHSLAIEKRSJQCKVLLVNGAN-----VHARAC 194
Db 70 NSSGD-----LMINCVD--VLGRNAVTTITENENDILQILLDYGGCSADMLVLAIDSEV 123
QY 195 G-----REFOKGQSTCFEFG-----LPLSLAATKQMDVSYLLE--- 230
Db 124 GAVDILLNHRRKRSRPTIVKMYERIQNPEXSTMDVAPVTLAHRNRYEITMLLKQDV 183
QY 231 ---NPH-----QPSAQDQDSQNTVLAHLVNI 255
Db 184 SLRPHAVGCECTLSAKNNKDSLHRSRFRIDYRCLASPAALLMLTEE--DPLRFEES 241

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QY 377 ---NKLQAKMDLIPKFLNLIYMEFTAVAYHPTLKOAPHLKA-----EV 427
 DB 572 AVHHNMLDVK--LLPR-----GGSPHSPAMNGTTPHIAKONQIEV 613
 QY 428 GNSMLTGG 435
 DB 614 ARSLLOYG 621

RESULT 8
 TRP3_HUMAN STANDARD; PRT; 848 AA.
 ID Q13507; O00593; O15660;
 AC 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DE 01-OCT-2000 (Rel. 40, Last annotation update)
 DE TRANSIENT RECEPTOR POTENTIAL CHANNEL 3 (HTRP-3).
 GN TRP3 OR TRP3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-96234226; PubMed-8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
 RA Birnbaumer L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RT Cell 85:661-671(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97358541; PubMed-9215637;
 RA Xu X.-Z., Li H.-S., Guggino W.B., Montell C.;
 RT "Coassembly of TRP and TRPL produces a distinct store-operated
 RT conductance.";
 RT Cell 89:1155-1164(1997).
 RN [3]
 RP SEQUENCE OF 632-747 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE-96003837; PubMed-7568191;
 RA Wes P.D., Chevesich J., Jeromin A., Rosenberg C., Stetten G.,
 RA Montell C.;
 RT "TRPC1, a human homolog of a Drosophila store-operated channel.";
 RT Proc. Natl. Acad. Sci. U.S.A. 92:9652-9656(1995).
 CC -1- FUNCTION: SUGGESTED TO MEDIATE CAPACITATIVE CALCIUM ENTRY (CCE).
 CC SEEMS TO FORM A CALCIUM PERMEANT CHANNEL.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 4 ANK REPEATS.
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 CC
 DR EMBL: U47050; AAC51653.1; -
 DR EMBL: Y13758; CAA74083.1; -
 DR EMBL: X89068; CAA61448.1; -
 DR MIM: 602345; -
 DR InterPro: IPR002110; -
 DR InterPro: IPR002111; -
 DR InterPro: IPR002153; -
 DR Pfam: PF00023; ank; 2;
 DR PRINTS: PR01097; TRNSRCEPTRP.
 KN Ionic channel; Transmembrane; Ion transport; Calcium channel;
 KN ANK repeat; Repeat; Glycoprotein.
 FT TRANSMEM 350 370 POTENTIAL.
 FT TRANSMEM 362 402 POTENTIAL.

FT TRANSMEM 431 451 POTENTIAL.
 FT TRANSMEM 464 484 POTENTIAL.
 FT TRANSMEM 536 556 POTENTIAL.
 FT TRANSMEM 580 600 POTENTIAL.
 FT TRANSMEM 616 636 POTENTIAL.
 FT TRANSMEM 650 670 POTENTIAL.
 FT REPEAT 38 67 ANK 1.
 FT REPEAT 73 102 ANK 2.
 FT REPEAT 104 130 ANK 3.
 FT REPEAT 159 188 ANK 4.
 FT CARBOHYD 337 337 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 403 403 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 560 560 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAc. . .) (POTENTIAL).
 FT CONFLICT 739 742 EMGM -> GNGEM (IN REF. 3).
 SQ SEQUENCE 848 AA; 97354 MW; 1DBC92BC941DE416 CRC64;

Query Match 3.5%; Score 139; DB 1; Length 848;

Best Local Similarity 18.4%; Pred. No. 0.024;

Matches 128; Conservative 96; Mismatches 222; Indels 248; Gaps 32;

QY 152 VNAOCTDYYRGHSALHIAIEKRSLOQVLLV--ENGAVY-----HAR----- 192
 DB 65 LVNVCVD--YMGONMLOLVAGNHELEVELLKKERLARGALLAISKGYRIVEAIL 122
 QY 193 -----ACGRFQKG-----OGNCFYFGLPLSLACTQKMDVSYLL-- 229
 DB 123 NHPGFAKRLTLSPCEQLDDDFRAYDEQGTRESPTDITPIILAAHCKEYEVHMLMK 182
 QY 230 ---ENPH-----OPASLOANDSOGNTVLAHV 253
 DB 183 GARIEPHDYFCCKGDCMEKORHDSFSHSRINAYKGLASPAVLSL--SSDPVLTAL 240
 QY 254 MISDMSAENIALVTSMYD-----GLLAGARLC-PRVQLEDIRN--LQDL 295
 DB 241 L--SHELAKIANIEKEFKNDYRKLSMOCKDFVGYLD--LCRDEEEVALINDLESA 294
 QY 296 TPPLKLAAGKGLIEFRH--ILOREFSGLSLHRSKPFEM--CYGPVRSYLDIASVDSCE 351
 DB 295 EPL-----EVHRKASLSRVKLAIEYVKKFAVHNCQOOLITTYE--NLSGLRE 343
 QY 352 NSVLEIIAIFHCKSPHRRHVVV-----EPLNKLQAKMDLIPKFL 393
 DB 344 ----QTIATKC-----LVVLVALGLPFLAIGVIAPCSRIGKILRSP-----FM 384
 QY 394 NPLCNLIYFITTAVAYHO-----PLKKQAPHLKAEVGNSSLTGHILIL-- 440
 DB 385 KEVAHAASPIIFLGLLVFNASDRFEGITTLPMITVTDYPRKQIFRKVTOFTWEMLIHW 444
 QY 441 -LGGIYLLVAGOLWY-----FMRHRYFI-----WISF-----IDSY 469
 DB 445 VLGMMSEKELMEGPREYIIQLANVLDLFGMLSTIFIAFTARFLAQLQATQAQYVDSY 504
 QY 470 FEILFLQALLTVVSQVLCFLAIEWLP-----LLVSALVIGWLLNLYYRGFOHT 520
 DB 505 VQESDLSEVTLPEIIOYFTYARDKW-LPSDPQIISGLVAIVVFSRIVAILPANESF 563
 QY 521 GIYSWIAQVILRDLRLPLLIYLVLFPGFAVALVLSQGAMPPEAPGTGNNAESVQPMG 580
 DB 564 GPLQISLGRTY-KDIFKEVNLFIWVFAFMIGMTILSYLQAKV----- 607
 QY 581 QEDEGGAQYRGILFASLELFKFTIGMGLA-----FOQLHFRGMVLLLLAYVL 631
 DB 608 -----NAFTVESSEFKLFFSIFGLSEVTSVLKDHKFIENIGY-----VLGIYIV 656
 QY 632 LTYILLNMLIAMSETVNSVATDSMSIWKLQKA 665
 DB 657 TMVVVLLNMLIAMINSVQEIEDSDVEKFKFARS 690

RESULT 9

| ID | ANK1_HUMAN | STANDARD: | PRT: 1880 AA. |
|----|--|-----------|---------------|
| AC | P16157; | | |
| DT | 01-APR-1990 (Rel. 14, Created) | | |
| DT | 01-APR-1990 (Rel. 14, Last sequence update) | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | |
| DE | ANKYRIN 1 (ERYTHROCYTE ANKYRIN) (ANKYRIN R) (ANKYRINS 2.1 AND 2.2). | | |
| GN | ANK1 OR ANK. | | |
| OS | Homo sapiens (Human). | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | |
| OX | NCBI_Taxid:9606; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND VARIANTS. | | |
| RC | TISSUE-Hematopoietic; | | |
| RX | MEDLINE=90158830; PubMed=2137557; | | |
| RX | Lux S.E., John K.M., Bennett V.; | | |
| RT | "Analysis of cDNA for human erythrocyte ankyrin indicates a repeated | | |
| RT | structure with homology to tissue-differentiation and cell-cycle | | |
| RT | control proteins."; | | |
| RL | Nature 344:36-42(1990). | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=90175370; PubMed=1689849; | | |
| RA | Lambert S., Yu H., Prechal J.T., Lawler J., Ruff P., Speicher D., | | |
| RA | Cheng M.C., Kan Y.W., Palek J.; | | |
| RT | "cDNA sequence for human erythrocyte ankyrin." | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990). | | |
| RN | [3] | | |
| RP | VARIANT HS ILE-462. | | |
| RX | MEDLINE=9625450; PubMed=8640229; | | |
| RA | Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T., | | |
| RA | Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A., | | |
| RA | Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.; | | |
| RT | "Ankyrin-1 mutations are a major cause of dominant and recessive | | |
| RT | hereditary spherocytosis." | | |
| RL | Nat. Genet. 13:214-218(1996). | | |
| CC | -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL | | |
| CC | ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO | | |
| CC | NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE | | |
| CC | CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN. | | |
| CC | ERYTHROCYTE ANKIRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE | | |
| CC | CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN; | | |
| CC | THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS. | | |
| CC | -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC | | |
| CC | PLASMA MEMBRANE. | | |
| CC | -1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY | | |
| CC | ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN | | |
| CC | VARIANT 2.1. | | |
| CC | -1- PTM: REGULATED BY PHOSPHORYLATION. | | |
| CC | -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S). | | |
| CC | -1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE | | |
| CC | HEREDITARY SPHEROCYTOSIS (HS). | | |
| CC | -1- SIMILARITY: CONTAINS 23 ANK REPEATS. | | |
| CC | ----- | | |
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| CC | or send an email to license@isb-sib.ch). | | |
| CC | ----- | | |
| DR | EMBL: X16609; CAA34610.1; - | | |
| DR | EMBL: M28880; AAA51732.1; - | | |
| DR | PIR: S08275; SJHUK. | | |
| DR | PIR: A35049; A35049. | | |
| DR | HSP: Q00420; IAMC. | | |
| DR | MIM: 182900; - | | |
| DR | InterPro: IPR000448; - | | |
| DR | InterPro: IPR000906; - | | |
| DR | InterPro: IPR002110; - | | |
| DR | Pfam: PF00791; Z05; 1. | | |

| | |
|----|---|
| DR | Pfam: PF00023; ank: 22. |
| DR | Pfam: PF00531; death: 1. |
| DR | PROSITE; PS50088; ANK_REPEAT: 20. |
| DR | PROSITE; PS50297; DEATH_DOMAIN: 1. |
| KW | Cytoskeleton; Alternative splicing; Repeat; ANK repeat; |
| KW | Phosphorylation; Lipoprotein; Multigene family; Disease mutation; |
| KM | Elliptocytosis; Polymorphism. |
| FT | DOMAIN 1 826 |
| FT | INT_MET 0- |
| FT | DOMAIN 827 1381 |
| FT | DOMAIN 1382 1880 |
| FT | REPEAT 43 72 |
| FT | REPEAT 76 105 |
| FT | REPEAT 109 138 |
| FT | REPEAT 142 171 |
| FT | REPEAT 173 200 |
| FT | REPEAT 204 233 |
| FT | REPEAT 237 266 |
| FT | REPEAT 270 299 |
| FT | REPEAT 303 332 |
| FT | REPEAT 336 365 |
| FT | REPEAT 369 398 |
| FT | REPEAT 402 431 |
| FT | REPEAT 435 464 |
| FT | REPEAT 468 497 |
| FT | REPEAT 501 530 |
| FT | REPEAT 534 563 |
| FT | REPEAT 567 596 |
| FT | REPEAT 600 629 |
| FT | REPEAT 633 662 |
| FT | REPEAT 666 695 |
| FT | REPEAT 699 728 |
| FT | REPEAT 732 761 |
| FT | REPEAT 765 794 |
| FT | DOMAIN 1402 1486 |
| FT | VARSPLIC 1512 1873 |
| FT | VARSPLIC 1874 1874 |
| FT | VARSPLIC 1849 1880 |
| FT | VARIANT 20 20 |
| FT | VARIANT 462 462 |
| FT | VARIANT 618 618 |
| FT | VARIANT 749 749 |
| FT | VARIANT 844 844 |
| FT | VARIANT 1391 1391 |
| FT | VARIANT 1285 1285 |
| FT | VARIANT 1591 1591 |
| FT | VARIANT 1698 1698 |
| FT | CONFLICT 229 229 |
| FT | CONFLICT 1345 1345 |
| FO | SEQUENCE 1880 AA: 206145 MW: 10555EYEPDICA28 CRC64: |

| | | | | |
|-----------------------|-----------------------|------------------------|-------|-----------------|
| Query Match | 3.4% | Score 138; | DB 1; | Length 1880; |
| Best Local Similarity | 22.8% | Pred. No. 0.079; | | |
| Matches | 82; | Conservative | 45; | Mismatches 122; |
| | | | | Indels 110; |
| | | | | Gaps 16; |
| OY | 134 CILPLQLQIDRD----- | SSNPQPL-VNAQCTDYR----- | ----- | GHSA LHI 169 |

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Db 319 CAVRLLOQDAEIDITLDTLPLHVAHC--GHHRAVAKVLLDKGAKPNSRALNGFTPLHI 376
QY 170 AIEKRSLQCKVLVENGANY-----HARAGRFQKG--QGTCTCYFG 209
Db 377 ACKNNHVRVELLTKGASIDAVTESGLTPLHVASFGHLPYKNNLLQKASPNVSNKV 436
QY 210 ELPPLSLACTKQMDVSYLLENPHQASLOATDSQNTVHALVMSIDNSAENIALVTSM 269
Db 437 ETPPLHMAARGHTEVAKYLLQ--KAKVNAKKADQTPPLHCAARIGH-----TNM 484
QY 270 YDGLLOAGARLCTVOLEDIRNLDTPLKLAKEGKIEIFRHILQREFSGLSLKRFT 329
Db 485 VKLLENNAN-----PNLATTAGHTPLHIAAREGHVETVLALKEKASQACMTKKGFT 537
QY 330 EW-----CYGVRYS---LYDLASVDSCEENSYLEI-IAFHCKSPHRHRMRYVLEPLNKLQ 381
Db 538 PLHVAAYGVRAVELLERDAHPNAGKNGPLPLHVAHV---HNNLDIV-----584
QY 382 AKMDLIPKFEFLNCLIMYFTAVAYHQPTLKKQAAPHLKA-----EVGNSMLLTG 435
Db 585 ---KILLIPR-----GGSPHSPPAMNGYTPPLHIAKQNOVEVARSLLQYG 624

RESULT 10
LATA_LATMA STANDARD; PRT; 1401 AA.
AC P23631:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE ALPHA-LATROTOXIN PRECURSOR.
OS Latrodectus mactans (Black widow spider).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Araneomorphae; Entelegynae; Araneidae; Theridiidae; Latrodectus.
OC NCBI_TaxId=6924;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-TREDECINGUTTATUS; TISSUE-Venom;
RX MEDLINE-91362695; PubMed-1888339;
RA Volkova T.M., Galkina T.G., Kudelin A.B., Nazimov I.V., Grishin E.V.;
RT "Structure of tryptic fragments of a neurotoxin from black widow
RT spider venom."
RL Bioorg. Khim. 17:437-441(1991).
CC -1- FUNCTION: CAUSES SYNAPTIC VESICLES EXOCYTOSIS AND
CC NEUROTRANSMITTER RELEASE FROM PRESYNAPTIC NERVE TERMINALS.
CC -1- PTM: ALPHA-LATROTOXIN MAY BE PROCESSED AT ITS C-TERMINUS.
CC -1- SIMILARITY: CONTAINS 21 ANK REPEATS.
DR PIR: S11527; S11527.
DR HSSP: Q00420; IAWC.
DR InterPro: IPR002110; -.
DR Pfam: PF00023; ank_17.
DR PROSITE: PS50088; ANK_REPEAT: 11.
DR PROSITE: PS50297; ANK_REGION: 1.
KW Toxin; Neurotoxin; Repeat; ANK repeat; Venom; Signal.
FT SIGNAL 1 20
FT CHAIN 21 1401 ALPHA-LATROTOXIN.
FT REPEAT 490 521 ANK 1.
FT REPEAT 525 554 ANK 2.
FT REPEAT 559 589 ANK 3.
FT REPEAT 593 622 ANK 4.
FT REPEAT 626 656 ANK 5.
FT REPEAT 660 690 ANK 6.
FT REPEAT 695 723 ANK 7.
FT REPEAT 729 758 ANK 8.
FT REPEAT 762 791 ANK 9.

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FT REPEAT 795 824 ANK 10.
FT REPEAT 828 857 ANK 11.
FT REPEAT 862 891 ANK 12.
FT REPEAT 895 924 ANK 13.
FT REPEAT 928 957 ANK 14.
FT REPEAT 971 1003 ANK 15.
FT REPEAT 1003 1033 ANK 16.
FT REPEAT 1035 1064 ANK 17.
FT REPEAT 1068 1097 ANK 18.
FT REPEAT 1101 1131 ANK 19.
FT REPEAT 1137 1166 ANK 20.
FT REPEAT 1170 1199 ANK 21.
SQ SEQUENCE 1401 AA; 156834 MW; 21CE198B80172568 CRC64;

Query Match 3.4%; Score 134.5; DB 1; Length 1401;
Best Local Similarity 20.1%; Pred. No. 0.097;
Matches 69; Conservative 62; Mismatches 123; Indels 89; Gaps 13;

QY 35 GLPPMESQFQGEGR---KFAQIRVNLNRYRGT-----GASOPD 70
Db 594 GTPPLHAIATNGERILEAFNLQISIDVNAKSNGLPPLHAIITKNDMPVASTLLGSKVD 653
QY 71 PNRFDRLFNVAVSQGVPEDLAQLPEYLSKTSKYTFDSEYTESGKTCLMK---AVLN 126
Db 654 INAVDENNI-----TALHYAAILGYLETTKOLINLKEINAVVSPGLLSALHYAIIY 706
QY 127 LKGVANACILPLQIDRDSNPQPLVNAOCTDYYGHSALHAIERSLQCKVLVENG 186
Db 707 KHDVASFELMRSSNVN-----VNLKALG---GTPPLHAIIVQGRKQILSTMFIDIG 753
QY 187 ANYHARACGRFQGGGTCEFGELPLSLACTKQMDVSYLLENPHQASLOATDSQGN 246
Db 754 VNIEQGTDEKY-----TPLHLAAMSKYPELIQILD---QGSNFEAKTNSGA 797
QY 247 TVLH-----ALVMSD-----NSAEN--TALVTSMYDGLQ-AGARLCTVOLED 288
Db 798 TPLHLATFKGSOAALILNLNENVMWRDDENGMPHIGAMTCLILVQAIIISIDATVVD 857
QY 289 IRLNQLDTPLKLAKEGKIEIFRHILQ-----REPSGSHL 324
Db 858 IEDKNSDTPLNLAONSHIDVITVFIDQCADITFRNKKGLAPL 900

RESULT 11
YAZA_SCHPO
ID YAZA_SCHPO STANDARD; PRT; 642 AA.
AC Q09701:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOHETICAL 72.5 KDA PROTEIN C2F7.10 IN CHROMOSOME 1.
GN SPAC2F7.10.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes.
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomyces.
OC NCBI_TaxId=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Gentles S., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (Jul-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: NO YEAST AKR1.
CC -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
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CC or send an email to license@sib.ch).
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| | | | | | |
|----|----------|------|------|----------------|------------------------------|
| FT | DOMAIN | 273 | 309 | EGF-LIKE 7, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 311 | 350 | EGF-LIKE 8, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 352 | 388 | EGF-LIKE 9, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 389 | 427 | EGF-LIKE 10, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 429 | 470 | EGF-LIKE 11, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 472 | 508 | EGF-LIKE 12, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 510 | 546 | EGF-LIKE 13, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 548 | 584 | EGF-LIKE 14, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 586 | 622 | EGF-LIKE 15, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 622 | 656 | EGF-LIKE 16, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 658 | 686 | EGF-LIKE 17, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 688 | 724 | EGF-LIKE 18, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 726 | 762 | EGF-LIKE 19, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 764 | 800 | EGF-LIKE 20, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 803 | 839 | EGF-LIKE 21, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 841 | 877 | EGF-LIKE 22, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 878 | 924 | EGF-LIKE 23, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 926 | 962 | EGF-LIKE 24, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 964 | 1000 | EGF-LIKE 25, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 1002 | 1040 | EGF-LIKE 26, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 1042 | 1081 | EGF-LIKE 27, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 1083 | 1122 | EGF-LIKE 28, | CALCIUM-BINDING (POTENTIAL). |
| FT | DOMAIN | 1126 | 1167 | EGF-LIKE 29, | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1168 | 1208 | LIN/NOTCH 1. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1209 | 1242 | LIN/NOTCH 2. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1243 | 1282 | LIN/NOTCH 3. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1628 | 1657 | ANK 1. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1661 | 1691 | ANK 2. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1695 | 1724 | ANK 3. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1728 | 1757 | ANK 4. | CALCIUM-BINDING (POTENTIAL). |
| FT | REPEAT | 1761 | 1790 | ANK 5. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 25 | 38 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 32 | 48 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 50 | 59 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 65 | 77 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 71 | 100 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 102 | 111 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 119 | 130 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 124 | 140 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 142 | 151 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 157 | 168 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 162 | 177 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 179 | 188 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 195 | 208 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 202 | 217 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 219 | 228 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 235 | 246 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 240 | 259 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 261 | 270 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 277 | 288 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 282 | 297 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 299 | 308 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 315 | 329 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 323 | 338 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 340 | 349 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 356 | 367 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 361 | 376 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 378 | 387 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 393 | 404 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 398 | 415 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 417 | 426 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 433 | 449 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 443 | 458 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 460 | 469 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 476 | 487 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 481 | 496 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 498 | 507 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 514 | 525 | BY SIMILARITY. | CALCIUM-BINDING (POTENTIAL). |
| FT | DISULFID | 519 | 534 | BY SIMILARITY. | CALCI |

| | | | | | | |
|----|----------|------|------|----|-------------|--|
| FT | DISULFID | 590 | 601 | BY | SIMILARITY. | |
| FT | DISULFID | 595 | 610 | BY | SIMILARITY. | |
| FT | DISULFID | 612 | 621 | BY | SIMILARITY. | |
| FT | DISULFID | 626 | 637 | BY | SIMILARITY. | |
| FT | DISULFID | 631 | 646 | BY | SIMILARITY. | |
| FT | DISULFID | 648 | 655 | BY | SIMILARITY. | |
| FT | DISULFID | 662 | 669 | BY | SIMILARITY. | |
| FT | DISULFID | 664 | 674 | BY | SIMILARITY. | |
| FT | DISULFID | 676 | 685 | BY | SIMILARITY. | |
| FT | DISULFID | 692 | 703 | BY | SIMILARITY. | |
| FT | DISULFID | 697 | 712 | BY | SIMILARITY. | |
| FT | DISULFID | 714 | 723 | BY | SIMILARITY. | |
| FT | DISULFID | 730 | 741 | BY | SIMILARITY. | |
| FT | DISULFID | 735 | 750 | BY | SIMILARITY. | |
| FT | DISULFID | 752 | 761 | BY | SIMILARITY. | |
| FT | DISULFID | 758 | 779 | BY | SIMILARITY. | |
| FT | DISULFID | 773 | 788 | BY | SIMILARITY. | |
| FT | DISULFID | 790 | 799 | BY | SIMILARITY. | |
| FT | DISULFID | 807 | 818 | BY | SIMILARITY. | |
| FT | DISULFID | 812 | 827 | BY | SIMILARITY. | |
| FT | DISULFID | 829 | 838 | BY | SIMILARITY. | |
| FT | DISULFID | 845 | 856 | BY | SIMILARITY. | |
| FT | DISULFID | 850 | 865 | BY | SIMILARITY. | |
| FT | DISULFID | 867 | 876 | BY | SIMILARITY. | |
| FT | DISULFID | 882 | 903 | BY | SIMILARITY. | |
| FT | DISULFID | 897 | 912 | BY | SIMILARITY. | |
| FT | DISULFID | 914 | 923 | BY | SIMILARITY. | |
| FT | DISULFID | 930 | 941 | BY | SIMILARITY. | |
| FT | DISULFID | 935 | 950 | BY | SIMILARITY. | |
| FT | DISULFID | 952 | 961 | BY | SIMILARITY. | |
| FT | DISULFID | 968 | 979 | BY | SIMILARITY. | |
| FT | DISULFID | 973 | 988 | BY | SIMILARITY. | |
| FT | DISULFID | 990 | 999 | BY | SIMILARITY. | |
| FT | DISULFID | 1006 | 1019 | BY | SIMILARITY. | |
| FT | DISULFID | 1011 | 1028 | BY | SIMILARITY. | |
| FT | DISULFID | 1030 | 1039 | BY | SIMILARITY. | |
| FT | DISULFID | 1046 | 1057 | BY | SIMILARITY. | |
| FT | DISULFID | 1051 | 1069 | BY | SIMILARITY. | |
| FT | DISULFID | 1071 | 1080 | BY | SIMILARITY. | |
| FT | DISULFID | 1087 | 1098 | BY | SIMILARITY. | |
| FT | DISULFID | 1092 | 1110 | BY | SIMILARITY. | |
| FT | DISULFID | 1112 | 1121 | BY | SIMILARITY. | |
| FT | DISULFID | 1130 | 1142 | BY | SIMILARITY. | |
| FT | DISULFID | 1136 | 1155 | BY | SIMILARITY. | |
| FT | DISULFID | 1157 | 1166 | BY | SIMILARITY. | |

Query Match

Best Local Similarity 3.2%; Score 129; DB 1; Length 1964;

Matches 72; Conservative 37; Mismatches 103; Indels 70; Gaps 12;

| | | | |
|----|------|---|------|
| Oy | 94 | LPEYLSKTSKYLTDSY-----TEGSTGKTCIMKAV-----LNKIDVNACTPLLOIDRDS | 145 |
| Db | 1553 | LPOQAMLPPOCESESEVLDPDTCGPDGYPLPMSAVFCGCGVOSTGASPORLGL----- | 1605 |
| Oy | 146 | GMPPO-----LVNAOCTDDYY--RGSHALHIALEKNSLQCVKLVENGAN----- | 188 |
| Db | 1606 | GLLEPWEPLLDGACPOAHVTGTEGPLTLARLFRSPTARLRLLEGANPNPPDAGRTP | 1665 |
| Oy | 189 | -----VHARACGRFFOKQGTCTF-----YFGEPLPLSLACTRQMDVSYLLENPHQOPASL | 238 |
| Db | 1666 | LHTAVALAADAREVCQOLLASRQTSVDARTEDGTPPLMLARLAVEDUEBLIA---ARADV | 1722 |
| Oy | 239 | QATDSQGNVTVLHALVWISDNSNSENTALALVTSMTDGLLOGARCLCPVVOLEDIRNLQDLPL | 298 |
| Db | 1723 | GARDRGKRTALMAAAYNNARA-----SLLOGAD-----KDAQDSREQTPPL | 1766 |
| Oy | 299 | KLAKEGKLEIFRHILQ-----REFSGLS---HLSRKPTW | 331 |
| Db | 1767 | FLAAREGAVEVAQULLELGAANGFLDQAGLADGVARQSRHW | 1808 |

RESULT 14

SW14_YEAST

| | | | |
|----|---|-----------|---------------|
| ID | SW14 YEAST | STANDARD: | PRT: 1093 AA. |
| AC | P25302: | | |
| DT | 01-MAY-1992 (rel. 22, Created) | | |
| DT | 01-FEB-1995 (rel. 31, Last sequence update) | | |
| DT | 01-OCT-2000 (rel. 40, Last annotation update) | | |
| DE | REGULATORY PROTEIN SW14 (CELL-CYCLE BOX FACTOR, CHAIN SW14) | | |
| DE | (APR1 PROTEIN). | | |
| GN | SW14 OR APR1 OR YER111C. | | |
| OS | Saccharomyces cerevisiae (Baker's yeast). | | |
| OC | Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | | |
| OC | Saccharomycetales; Saccharomycetaceae; Saccharomyces. | | |
| OX | NCBI_TaxID=49332; | | |
| RP | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RX | MEDLINE=90098089; PubMed=2689885; | | |
| RA | Andrews B.J., Herskowitz I.; | | |
| RT | "The yeast SW14 protein contains a present in developmental | | |
| RT | regulators and is part of a complex involved in cell-cycle-dependent | | |
| RL | transcription."; | | |
| RL | Nature 342:830-833(1989). | | |
| RN | [2] | | |
| RN | SEQUENCE FROM N.A. | | |
| RC | STRAIN=5288C / AB972; | | |
| RA | Dierich F.S., Mulligan J.F., Hennessey K.M., Allen E., Araujo R., | | |
| RA | Aviles E., Berro A., Brennan T., Carpenter J., Chen E., Cherry J.M., | | |
| RA | Chung E., Duncan M., Guzman E., Hartwell G., Hunnicke-Smith S., | | |
| RA | Hymn R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., | | |
| RA | Mosdale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C., | | |
| RA | Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., | | |
| RA | Taylor P., Wei Y., Yelton M., Botstein D., Davis R.M.; | | |
| RL | Submitted (DEC-1994) to the EMBL/Genbank/DBJ databases. | | |
| RN | [3] | | |
| RP | SEQUENCE OF 845-1093 FROM N.A. | | |
| RX | MEDLINE=93360904; PubMed=8355657; | | |
| RA | Daniel J.; | | |
| RT | "Potentially rapid walking in cellular regulatory networks using the | | |
| RT | gene-gene interference method in yeast."; | | |
| RL | Mol. Gen. Genet. 240:245-257(1993). | | |
| CC | -I- FUNCTION: PART OF A COMPLEX INVOLVED IN CELL-CYCLE-DEPENDENT | | |
| CC | TRANSCRIPTION. SW14 AND SW16 ARE REQUIRED FOR FORMATION OF THE | | |
| CC | CELL-CYCLE BOX FACTOR-DNA COMPLEX. THE REPEATED ELEMENT IN THE | | |
| CC | UPSTREAM REGION OF HO (5'-CACGAAA-3') IS CALLED THE CELL CYCLE | | |
| CC | BOX (CCB). | | |
| CC | -I- SUBUNIT: SBP CONTAINS SW16 AND SW14. | | |
| CC | -I- SIMILARITY: CONSTRAINTS 2 ANK REPEATS. | | |
| CC | ----- | | |
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| CC | or send an email to license@sib-sib.ch). | | |
| CC | ----- | | |
| DR | EMBL: X51606; CAA35949.1; - | | |
| DR | EMBL: U18916; AAC03209.1; - | | |
| DR | PIR: S07106; S07106. | | |
| DR | PIR: S35260; S35260. | | |
| DR | TRANSFAC: T00775; - | | |
| DR | SGD: S0000913; SW14. | | |
| DR | InterPro: IPR002110; - | | |
| DR | Pfam: PF00023; ank; 2. | | |
| DR | PROSITE: PS50088; ANK_REPEAT; 2. | | |
| DR | PROSITE: PS50297; ANK_REPEAT_REGION; 2. | | |
| KW | Transcription regulation; DNA-binding; ANK repeat; Repeat. | | |
| FT | DNA BIND | 37 | 138 |
| FT | DOMAIN | 201 | 727 |
| FT | REPEAT | 520 | 549 |
| FT | REPEAT | 641 | 670 |
| FT | CONFLICT | 175 | 175 |
| FT | CONFLICT | 431 | 431 |
| FT | CONFLICT | 1054 | 1054 |
| FT | CONFLICT | 3 | 846 |
| FT | MISSING (IN REF. 2). | | |

| Seq | SEQUENCE | 1093 AA: | 123806 MW: | 40EA2EA7732687A9 CRC64: |
|-----------------------|---|--|-----------------|-------------------------|
| Query Match | | 3.28; | Score 128.5; | DB 1; Length 1093; |
| Best Local Similarity | | 20.8%; | Pred. No. 0.19; | |
| Matches 74; | | Conservative 48; | Mismatches 134; | Indels 99; Gaps |
| Qy | 10 | FRLEFLDGGGDEGSEADRGKIDPFSSGLPRMSSQPGGDEKRFAPQIRV----- | 56 | |
| Db | 357 | FNHSMDSITNGNSKKRRKKTKINQSN-----EQDFYNOQEKIQRHFKKLMKQPLLMQSFQNP | 411 | |
| Oy | 57 | -----NLNRYKGTGASQDPDRPFDRDRLFNVAVSRGVEEDLAGLPEYLSKT | 101 | |
| Db | 412 | NDHNHEYCDNSGNNNNNTVAVSSSSIEVPSSENDSMMKSSMTPPFSAGNTSSQNKL | 471 | |
| Oy | 102 | SKYLTDSEYTEGSGTGKTCMLKAVLNLDGVNACILPLLQIDRDSGNQPL----- | 151 | |
| Db | 472 | ENKMTDQYKQ-----TILFTLSSRSRSDVDQALLATLALYPAPKN | 510 | |
| Oy | 152 | --VNAQCTDDYIRGHSAHLHIAIEKRSIQCVKVLVENGANVAHARCGRF-FQKGQGTCTFYF | 208 | |
| Db | 511 | FNINFEID--QCHTPLMWTAMANIPIKLMLITTLNAN--ALQCNKIGFNCITKYSIFVN | 565 | |
| Oy | 209 | GELPLSLAACKQ--MPVSVLLLENPHQPSLATQDSQGNVTVALMWDNSAENALV | 266 | |
| Db | 566 | N-----CKENAFDEIISILK-----ICLTIPDVNGRLPFHYLIELSVMKSNMTI | 612 | |
| Oy | 267 | TSMYDG-LLAGQ-----ARLCPTVOLEDIRNLQDLTPPLKLAKEGKIEIFRHIL | 314 | |
| Db | 613 | KSYMDSITLSGGQDYNLKTKCLWYQ-DNIGN-----TPHLSALNLFVEYNNRLV | 662 | |
| RESULT 15 | | | | |
| NOTCH_DROME | | STANDARD; | PRT; | 2703 AA. |
| AC | P07207; | P04154; | | |
| DT | 01-NOV-1986 (Rel. 03, Created) | | | |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update) | | | |
| DT | 01-OCT-2000 (Rel. 40, Last annotation update) | | | |
| DE | NEUROGENIC LOCUS NOTCH PROTEIN PRECURSOR. | | | |
| GN | N. | | | |
| OS | Drosophila melanogaster (Fruit fly). | | | |
| OC | Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; | | | |
| OC | Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; | | | |
| OC | Ephydrioidae; Drosophilidae; Drosophila. | | | |
| OX | NCBI_TaxID=7227; | | | |
| RN | [1] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RX | MEDLINE=66079539; PubMed=3935325; | | | |
| RA | Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.; | | | |
| RT | "Nucleotide sequence from the neurogenic locus notch implies a gene | | | |
| RT | product that shares homology with proteins containing EGF-like | | | |
| RT | repeats."; | | | |
| RL | Cell 43:567-581(1985). | | | |
| RL | [2] | | | |
| RN | SEQUENCE FROM N.A. | | | |
| RN | STRAIN=OREGON-R; | | | |
| RX | MEDLINE=87064624; PubMed=3097517; | | | |
| RA | Kidd S., Kelley M.R., Young M.W.; | | | |
| RT | "Sequence of the notch locus of Drosophila melanogaster: relationship | | | |
| RT | of the encoded protein to mammalian clotting and growth factors."; | | | |
| RL | Mol. Cell. Biol. 6:3094-3108(1986). | | | |
| RL | [3] | | | |
| RN | SEQUENCE OF 2505-2611 FROM N.A. | | | |
| RX | MEDLINE=85099329; PubMed=2981631; | | | |
| RA | Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.; | | | |
| RT | "opa: a novel family of transcribed repeats shared by the Notch locus | | | |
| RT | and other developmentally regulated loci in D. melanogaster."; | | | |
| RL | Cell 40:55-62(1985). | | | |
| RN | [4] | | | |
| RN | SEQUENCE OF 1-8 FROM N.A. | | | |
| RX | MEDLINE=87257846; PubMed=3037327; | | | |
| RA | Kelley M.R., Kidd S., Berg R.L., Young M.W.; | | | |

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RT      "Restriction of P-element insertions at the Notch locus of Drosophila
RT      melanogaster.";
RT      Mol. Cell. Biol. 7:1545-1548(1987).
RN      [5]
RP      REVIEW.
RA      Harris W.A.;
RT      "Many cell types specified by Notch function.";
RT      Curr. Biol. 1:120-122(1991).
CC      -1- FUNCTION: NOTCH PROTEIN IS ESSENTIAL FOR PROPER DIFFERENTIATION OF
CC      ECTODERM.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- MISCELLANEOUS: SEPARATION OF NEUROBLASTS FROM THE ECTODERM INTO
CC      THE INNER PART OF EMBRYO IS ONE OF THE FIRST STEPS OF CNS
CC      DEVELOPMENT IN INSECTS, THIS PROCESS IS UNDER CONTROL OF THE
CC      NEUROGENIC GENES.
CC      -1- SIMILARITY: HIGH, WITH OTHER NOTCH-TYPE PROTEINS.
CC      -1- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC      -1- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC      -----
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CC      -----
DR      EMBL: M16152; AAB59220.1; -
DR      EMBL: M16153; AAB59220.1; JOINED.
DR      EMBL: M16149; AAB59220.1; JOINED.
DR      EMBL: M16150; AAB59220.1; JOINED.
DR      EMBL: M16151; AAB59220.1; JOINED.
DR      EMBL: K03508; AAA28725.1; -
DR      EMBL: M13689; AAA28725.1; JOINED.
DR      EMBL: K03507; AAA28725.1; JOINED.
DR      EMBL: M12175; AAA74496.1; -
DR      EMBL: M16025; AAA28726.1; -
DR      PIR: A24420; A24420.
DR      PIR: A24768; A24768.
DR      PIR: A05267; A05267.
DR      HSSP: P00740; 1TXA.
DR      Flybase: FBgn0004647; N.
DR      InterPro: IPR000152; -
DR      InterPro: IPR000561; -
DR      InterPro: IPR000800; -
DR      InterPro: IPR001438; -
DR      InterPro: IPR001881; -
DR      InterPro: IPR002110; -
DR      Pfam: PF00008; EGF; 36.
DR      Pfam: PF00023; ank; 6.
DR      Pfam: PF00066; notch; 3.
DR      PRINTS: PR00010; EGFBLD.
DR      PROSITE: PS50086; ANK_REPEAT; 5.
DR      PROSITE: PS50297; ANK_REPEAT_REGION; 1.
DR      PROSITE: PS00010; ASX_HYDROXYL; 22.
DR      PROSITE: PS00022; EGF_1; 34.
DR      PROSITE: PS01186; EGF_2; 28.
DR      PROSITE: PS01187; EGF_CA; 22.
KW      Differentiation; Neurogenesis; Repeat; ANK repeat; EGF-like domain;
KW      Transmembrane; Signal; Glycoprotein.
FT      SIGNAL 1 44
FT      CHAIN 45 2703
FT      DOMAIN 45 1745
FT      TRANSMEM 1746 1766
FT      DOMAIN 1767 2703
FT      DOMAIN 58 95
FT      DOMAIN 96 136
FT      DOMAIN 139 176
FT      DOMAIN 177 215
FT      DOMAIN 217 253
FT      DOMAIN 255 291
FT      DOMAIN 293 329
FT      EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
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FT      EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 19, CALCIUM-BINDING (POTENTIAL).
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FT      EGF-LIKE 21, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 22, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 23, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 24, CALCIUM-BINDING (POTENTIAL).
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FT      EGF-LIKE 41, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 42, CALCIUM-BINDING (POTENTIAL).
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FT      EGF-LIKE 44, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 45, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 46, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 47, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 48, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 49, CALCIUM-BINDING (POTENTIAL).
FT      EGF-LIKE 50, CALCIUM-BINDING (POTENTIAL).

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| FT | DISULFID | 497 | 512 | BY SIMILARITY. |
| FT | DISULFID | 514 | 523 | BY SIMILARITY. |
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| FT | DISULFID | 665 | 674 | BY SIMILARITY. |
| FT | DISULFID | 681 | 692 | BY SIMILARITY. |

Query Match 3.1%; Score 124.5; DB 1; Length 2703;
 Best Local Similarity 23.9%; Pred. No. 1.2; Mismatches 15;
 Matches 75; Conservative 47; Indels 77; Gaps 15;

| | | | |
|----|------|---|------|
| QY | 39 | MESQEGEDRKFPQIRVNLNRYKRG--TGASQDPNRFDRD-----LFNAVSRG-- | 86 |
| DB | 1856 | MVSEYEADQRWSSQAHLDVVYVRAIMTPRAHQDGGKHVDARGPGCLTPIMIAAVRGCG | 1915 |
| QY | 87 | --VPEDLAGPEYLSKTSKYLD-----SEYEGSTGKTCIMKAVLNKQGVNACILP | 137 |
| DB | 1916 | LPTGEDIEENNED--STAQVISDLAOGAELNATMTKGTETSIHLAARFARADAAKRL- | 1971 |
| QY | 138 | LQIDRDGNGPQPLVNAOCTDYYRGHSALHIAIEKRSLOCVKLIYENG- NVHARACGR | 196 |
| DB | 1972 | -----DAG-----ADANCODN--TGRTPLHAVAADAGVFOILRNRAITNLNAR---- | 2014 |
| QY | 197 | FQKGGGTCFYEGELPLSLAACKQMDVVSYLENPHOPASLOATDSOGNTVLAHLMIS | 256 |
| DB | 2015 | -----MHDGTPPLILAARLAIEGWEDLIT--ADADRMAADNSGKTALHMAAVN | 2062 |
| QY | 257 | DNSAENIALVTSMYDGLLAGARLCPTVOLEDIRNLQDLTPLKLAKKEGKIETFRHIL-- | 314 |
| DB | 2063 | NTEAVNI-----LNMHHN-----RDQDDKDETPLELAREGSYECACKALDN | 2106 |
| QY | 315 | --QREFSGLSLSR | 326 |
| DB | 2107 | FANREIT--DHMDR | 2118 |

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 Job time: 131 sec